WHAT IS CLAIMED IS:

1. A method of determining the affinity between polypeptide amino acid residues and one or more molecular fragments comprising:

(a) conducting a computer simulation of (i) a polypeptide, and (ii) at least one molecular fragment, wherein at least one interaction energy is calculated between said polypeptide and said at least one molecular fragment, wherein said at least one calculated interaction energy is associated with a position of said at least one molecular fragment; and

(b) assigning an affinity value to at least one fragment and residue pair when said fragment is in the vicinity of the residue, wherein said affinity value is a measure of the free energy of interaction between the polypeptide and the fragment;

wherein (a) and (b) are conducted for each molecular fragment present in the computer simulation.

2. The method of claim 1, wherein said at least one fragment is defined as being in the vicinity of a residue when at least one pair of fragment-residue atoms is within a predetermined threshold distance, wherein said threshold distance is based on the sum of the Van der Waals radii of said fragment-residue atoms.

3. The method of claim 2, wherein said predetermined threshold distance is defined as:

$$r_{ij} < \alpha(R_{VdW,i} + R_{VdW,j}),$$

wherein r_{ij} is the distance between the two atoms, R_{VdW} is the Van der Waals radius and α is a numerical parameter.

4. The method of claim 3, wherein said α is between about 0.5 and about 2.0.

5. The method of claim 4, wherein said α is about 1.2.

6. The method of claim 3, wherein said Van der Waals radius is about half the Lennard-Jones parameter from a molecular mechanics force-field.

7. The method of claim 6, wherein said molecular mechanics force field is selected from the group consisting of AMBER, GROMOS, CHARMM, Xplor, Discover, MMFFF and Tripos.

8. The method of claim 7, wherein said molecular mechanics force field is the AMBER force field.

9. The method of claim 8, wherein said affinity value comprises B-critical, wherein B critical is defined as the minimum B value for which a particular fragment is persistently observed in the vicinity of a residue, wherein $B = \mu'/kT + \ln\langle N\rangle$, where μ' is the excess chemical potential, k is the Boltzmann's constant, T is the absolute temperature, and $\langle N\rangle$ is the mean number of molecules of the molecular fragment.

10. The method of claim 9, wherein a particular type of fragment is persistently observed in the vicinity of a residue when the average number of fragments in the vicinity of the residue is between 0.8 and 1.0.

11. The method of claim 10, wherein a particular type of fragment is persistently observed in the vicinity of a residue when the average number of fragments in the vicinity is greater than or equal to 0.9.

12. The method of claim 8, wherein said affinity values comprise B-critical, wherein B critical is defined as

$$B_c = -\log\left[\frac{1}{n_{\text{snap}}}\sum_{i=1}^{n_{\text{snap}}}\sum_{\text{frag j}\in\Delta V_b} e^{-B_{\text{num}}(Y_j)}\right];$$

wherein n_{snap} is a positive integer representing the number of snapshots from the numerical fragment density distribution, wherein $B_{num}(Y_j)$ is a field in the single particle configuration space Y, wherein said field represents an energy cost for a particular particle to leave the system from position Y; and $)V_b$ is the binding volume.

13. The method of claim 1, further comprising outputting a binding analysis profile, wherein said binding analysis profile comprises a matrix of affinity values for each fragment-residue pair.

14. The method of claim 1, wherein (a) and (b) are repeated for a plurality of fragment types.

15. The method of claim 14, wherein a matrix of affinity values are averaged over fragments types, and the polypeptide surface is coded according to fragment binding affinity.

16. The method of claim 15, wherein residues with highest fragment binding affinity values are displayed with a different color from the residues with the lowest affinity value.